#2   OIPE

DATE: 04/26/2001
TIME: 10:40:02

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/802,741

Input Set : N:\Crf3\RULE60\09802741.txt
Output Set: N:\CRF3\04262001\I802741.raw

ENTERED

SEQUENCE LISTING

```
C-->  3 (1) GENERAL INFORMATION:
      5       (i) APPLICANT: Fisher, Douglas A.
      6                      Gooding, Doug
      7                      Streeter, Dave
C-->  9     (ii) TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
     11    (iii) NUMBER OF SEQUENCES: 14
     13     (iv) CORRESPONDENCE ADDRESS:
     14         (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
     15         (B) STREET: 3174 Porter Dr.
     16         (C) CITY: Palo Alto
     17         (D) STATE: CA
     18         (E) COUNTRY: USA
     19         (F) ZIP: 94304
     21      (v) COMPUTER READABLE FORM:
     22         (A) MEDIUM TYPE: Diskette
     23         (B) COMPUTER: IBM Compatible
     24         (C) OPERATING SYSTEM: DOS
     25         (D) SOFTWARE: FastSEQ for Windows Version 2.0
     27     (vi) CURRENT APPLICATION DATA:
C--> 28         (A) APPLICATION NUMBER: US/09/802,741
C--> 29         (B) FILING DATE: 08-Mar-2001
     30         (C) CLASSIFICATION:
     32    (vii) PRIOR APPLICATION DATA:
     33         (A) APPLICATION NUMBER: 09/240,359
     34         (B) FILING DATE:
     37   (viii) ATTORNEY/AGENT INFORMATION:
     38         (A) NAME: Billings, Lucy J.
     39         (B) REGISTRATION NUMBER: 36,749
     40         (C) REFERENCE/DOCKET NUMBER: PF-0442 US
     42     (ix) TELECOMMUNICATION INFORMATION:
     43         (A) TELEPHONE: 650-855-0555
     44         (B) TELEFAX: 650-845-4166
     47 (2) INFORMATION FOR SEQ ID NO: 1:
     49       (i) SEQUENCE CHARACTERISTICS:
     50         (A) LENGTH: 593 amino acids
     51         (B) TYPE: amino acid
     52         (C) STRANDEDNESS: single
     53         (D) TOPOLOGY: linear
     55     (vii) IMMEDIATE SOURCE:
     56         (A) LIBRARY: PROSNOT06
     57         (B) CLONE: 828228
     59      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     62 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
     63  1               5                  10                  15
     64 Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
     65              20                  25                  30
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4/26/01

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66   Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
67            35                  40                  45
68   Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
69            50                  55                  60
70   Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
71   65                  70                  75                  80
72   Val Ala Ile Lys Gln Leu Ser Ala Gly Val Glu Asp Lys Arg Thr Thr
73                    85                  90                  95
74   Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg Arg Val Val
75                  100                 105                 110
76   Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser Gly Gln Val
77            115                 120                 125
78   Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu Gly Gln Arg
79            130                 135                 140
80   Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
81   145                 150                 155                 160
82   Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
83                  165                 170       .         175
84   Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly
85                  180                 185                 190
86   Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met
87            195                 200                 205
88   Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys
89            210                 215                 220
90   Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val
91   225                 230                 235                 240
92   Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu
93                  245                 250                 255
94   Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu
95                  260                 265                 270
96   Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe
97            275                 280                 285
98   Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp
99   290                 295                 300
100  Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val
101  305                 310                 315                 320
102  Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys
103                  325                 330                 335
104  Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His
105                  340                 345                 350
106  Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg
107            355                 360                 365
108  Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His
109            370                 375                 380
110  His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
111  385                 390                 395                 400
112  Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
113                  405                 410                 415
114  Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
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115                420              425              430
116  Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
117         435              440              445
118  His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
119      450              455              460
120  Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
121  465              470              475              480
123  Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu
124              485              490              495
125  Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala
126           500              505              510
127  Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val
128         515              520              525
129  Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp
130      530              535              540
131  Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met
132  545              550              555              560
133  Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu
134              565              570              575
135  Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys
136              580              585              590
137  Ala
140  (2) INFORMATION FOR SEQ ID NO: 2:
142       (i) SEQUENCE CHARACTERISTICS:
143             (A) LENGTH: 1997 base pairs
144             (B) TYPE: nucleic acid
145             (C) STRANDEDNESS: single
146             (D) TOPOLOGY: linear
148      (vii) IMMEDIATE SOURCE:
149             (A) LIBRARY: PROSNOT06
150             (B) CLONE: 828228
152       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
154  GCTCCCCGCG GCGGCTGGCG TCGGGAAAGT ACAGTAAAAA GTCCGAGTGC AGCCGCCGGG    60
155  CGCAGGATGG GATCCGGCTC CTCCAGCTAC CGGCCCAAGG CCATCTACCT GGACATCGAT   120
156  GGACGCATTC AGAAGGTAAT CTTCAGCAAG TACTGCAACT CCAGCGACAT CATGGACCTG   180
157  TTCTGCATCG CCACCGGCCT GCCTCGGAAC ACGACCATCT CCCTGCTGAC CACCGACGAC   240
158  GCCATGGTCT CCATCGACCC CACCATGCCC GCGAATTCAG AACGCACTCC GTACAAAGTG   300
159  AGACCTGTGG CCATCAAGCA ACTCTCCGCT GGTGTCGAGG ACAAGAGAAC CACAAGCCGT   360
160  GGCCAGTCTG CTGAGAGACC ACTGAGGGAC AGACGGGTTG TGGGCCTGGA GCAGCCCCGG   420
161  AGGGAAGGAG CATTTGAAAG TGGACAGGTA GAGCCCAGGC CCAGAGAGCC CCAGGGCTGC   480
162  TACCAGGAAG GCCAGCGCAT CCCTCCAGAG AGAGAAGAAT TAATCCAGAG CGTGCTGGCG   540
163  CAGGTTGCAG AGCAGTTCTC AAGAGCATTC AAAATCAATG AACTGAAAGC TGAAGTTGCA   600
164  AATCACTTGG CTGTCCTAGA GAAACGCGTG GAATTGGAAG GACTAAAAGT GGTGGAGATT   660
165  GAGAAATGCA AGAGTGACAT TAAGAAGATG AGGGAGGAGC TGGCGGCCAG AAGCAGCAGG   720
166  ACCAACTGCC CCTGTAAGTA CAGTTTTTTG GATAACCACA AGAAGTTGAC TCCTCGACGC   780
167  GATGTTCCCA CTTACCCCAA GTACCTGCTC TCTCCAGAGA CCATCGAGGC CCTGCGGGAAG   840
168  CCGACCTTTG ACGTCTGGCT TTGGGAGCCC AATGAGATGC TGAGCTGCCT GGAGCACATG   900
169  TACCACGACC TCGGGCTGGT CAGGGACTTC AGCATCAACC CTGTCACCCT CAGGAGGTGG   960
170  CTGTTCTGTG TCCACGACAA CTACAGAAAC AACCCCTTCC ACAACTTCCG GCACTGCTTC  1020
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RAW SEQUENCE LISTING   DATE: 04/26/2001
PATENT APPLICATION: US/09/802,741   TIME: 10:40:02

Input Set : N:\Crf3\RULE60\09802741.txt
Output Set: N:\CRF3\04262001\I802741.raw

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171   TGCGTGGCCC AGATGATGTA CAGCATGGTC TGGCTCTGCA GTCTCCAGGA GAAGTTCTCA   1080
172   CAAACGGATA TCCTGATCCT AATGACAGCG GCCATCTGCC ACGATCTGGA CCATCCCGGC   1140
173   TACAACAACA CGTACCAGAT CAATGCCCGC ACAGAGCTGG CGGTCCGCTA CAATGACATC   1200
174   TCACCGCTGG AGAACCACCA CTGCGCCGTG GCCTTCCAGA TCCTCGCCGA GCCTGAGTGC   1260
175   AACATCTTCT CCAACATCCC ACCTGATGGG TTCAAGCAGA TCCGACAGGG AATGATCACA   1320
176   TTAATCTTGG CCACTGACAT GGCAAGACAT GCAGAAATTA TGGATTCTTT CAAAGAGAAA   1380
177   ATGGAGAATT TTGACTACAG CAACGAGGAG CACATGACCC TGCTGAAGAT GATTTTGATA   1440
178   AAATGCTGTG ATATCTCTAA CGAGGTCCGT CCAATGGAAG TCGCAGAGCC TTGGGTGGAC   1500
179   TGTTTATTAG AGGAATATTT TATGCAGAGC GACCGTGAGA AGTCAGAAGG CCTTCCTGTG   1560
180   GCACCGTTCA TGGACCGAGA CAAAGTGACC AAGGCCACAG CCCAGATTGG GTTCATCAAG   1620
181   TTTGTCCTGA TCCCAATGTT TGAAACAGTG ACCAAGCTCT TCCCCATGGT TGAGGAGATC   1680
182   ATGCTGCAGC CACTTTGGGA ATCCCGAGAT CGCTACGAGG AGCTGAAGCG GATAGATGAC   1740
183   GCCATGAAAG AGTTACAGAA GAAGACTGAC AGCTTGACGT CTGGGGCCAC CGAGAAGTCC   1800
184   AGAGAGAGAA GCAGAGATGT GAAAAACAGT GAAGGAGACT GTGCCTGAGG AAAGCGGGGG   1860
185   GCGTGGCTGC AGTTCTGGAC GGGCTGGCCG AGCTGCGCGG GATCCTTGTG CAGGGAAGAG   1920
186   CTGCCCTGGG CACCTGGCAC CACAAGACCA TGTTTTCTAA GAACCATTTT GTTCACTGAT   1980
187   ACAAAAAAAA AAAAAAA                                                   1997
189   (2) INFORMATION FOR SEQ ID NO: 3:
191        (i) SEQUENCE CHARACTERISTICS:
192            (A) LENGTH: 713 amino acids
193            (B) TYPE: amino acid
194            (C) STRANDEDNESS: single
195            (D) TOPOLOGY: linear
197       (vii) IMMEDIATE SOURCE:
198            (A) LIBRARY: THP1PLB02
199            (B) CLONE: 156196
201        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
203   Leu Ala Cys Phe Leu Asp Lys His His Asp Ile Ile Ile Ile Asp His
204   1               5                   10                  15
205   Arg Asn Pro Arg Gln Leu Asp Ala Glu Ala Leu Cys Arg Ser Ile Arg
206               20                  25                  30
207   Ser Ser Lys Leu Ser Glu Asn Thr Val Ile Val Gly Val Val Arg Arg
208           35                  40                  45
209   Val Asp Arg Glu Glu Leu Ser Val Met Pro Phe Ile Ser Ala Gly Phe
210       50                  55                  60
211   Thr Arg Arg Tyr Val Glu Asn Pro Asn Ile Met Ala Cys Tyr Asn Glu
212   65                  70                  75                  80
213   Leu Leu Gln Leu Glu Phe Gly Glu Val Arg Ser Gln Leu Lys Leu Arg
214               85                  90                  95
215   Ala Cys Asn Ser Val Phe Thr Ala Leu Glu Asn Ser Glu Asp Ala Ile
216               100                 105                 110
217   Glu Ile Thr Ser Glu Asp Arg Phe Ile Gln Tyr Ala Asn Pro Ala Phe
218           115                 120                 125
219   Glu Thr Thr Met Gly Tyr Gln Ser Gly Glu Leu Ile Gly Lys Glu Leu
220       130                 135                 140
221   Gly Glu Val Pro Ile Asn Glu Lys Lys Ala Asp Leu Leu Asp Thr Ile
222   145                 150                 155                 160
223   Asn Ser Cys Ile Arg Ile Gly Lys Glu Trp Gln Gly Ile Tyr Tyr Ala
224               165                 170                 175
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225  Lys Lys Lys Asn Gly Asp Asn Ile Gln Gln Asn Val Lys Ile Ile Pro
226          180                 185                 190
227  Val Ile Gly Gln Gly Gly Lys Ile Arg His Tyr Val Ser Ile Ile Arg
228          195                 200                 205
229  Val Cys Asn Gly Asn Asn Lys Ala Glu Lys Ile Ser Glu Cys Val Gln
230      210                 215                 220
231  Ser Asp Thr Arg Thr Asp Asn Gln Thr Gly Lys His Lys Asp Arg Arg
232  225                 230                 235                 240
233  Lys Gly Ser Leu Asp Val Lys Ala Val Ala Ser Arg Ala Thr Glu Val
234              245                 250                 255
235  Ser Ser Gln Arg Arg His Ser Ser Met Ala Arg Ile His Ser Met Thr
236              260                 265                 270
237  Ile Glu Ala Pro Ile Thr Lys Val Ile Asn Val Ile Asn Ala Ala Gln
238      275                 280                 285
239  Glu Ser Ser Pro Met Pro Val Thr Glu Ala Leu Asp Arg Val Leu Glu
240      290                 295                 300
241  Ile Leu Arg Thr Thr Glu Leu Tyr Ser Pro Gln Phe Gly Ala Lys Asp
242  305                 310                 315                 320
243  Asp Asp Pro His Ala Asn Asp Leu Val Gly Gly Leu Met Ser Asp Gly
244              325                 330                 335
245  Leu Arg Arg Leu Ser Gly Asn Glu Tyr Val Leu Ser Thr Lys Asn Thr
246              340                 345                 350
247  Gln Met Val Ser Ser Asn Ile Ile Thr Pro Ile Ser Leu Asp Asp Val
248      355                 360                 365
249  Pro Pro Arg Ile Ala Arg Ala Met Glu Asn Glu Glu Tyr Trp Asp Phe
250      370                 375                 380
251  Asp Ile Phe Glu Leu Glu Ala Ala Thr His Asn Arg Pro Leu Ile Tyr
252  385                 390                 395                 400
253  Leu Gly Leu Lys Met Phe Ala Arg Phe Gly Ile Cys Glu Phe Leu His
254              405                 410                 415
255  Cys Ser Glu Ser Thr Leu Arg Ser Trp Leu Gln Ile Ile Glu Ala Asn
256              420                 425                 430
257  Tyr His Ser Ser Asn Pro Tyr His Asn Ser Thr His Ser Ala Asp Val
258      435                 440                 445
259  Leu His Ala Thr Ala Tyr Phe Leu Ser Lys Glu Arg Ile Lys Glu Thr
260      450                 455                 460
261  Leu Asp Pro Ile Asp Glu Val Ala Ala Leu Ile Ala Ala Thr Ile His
262  465                 470                 475                 480
263  Asp Val Asp His Pro Gly Arg Thr Asn Ser Phe Leu Cys Asn Ala Gly
264              485                 490                 495
265  Ser Glu Leu Ala Ile Leu Tyr Asn Asp Thr Ala Val Leu Glu Ser His
266          500                 505                 510
267  His Ala Ala Leu Ala Phe Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn
268          515                 520                 525
269  Ile Phe Lys Asn Met Glu Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly
270      530                 535                 540
271  Ile Ile Asp Met Val Leu Ala Thr Glu Met Thr Lys His Phe Glu His
272  545                 550                 555                 560
273  Val Asn Lys Phe Val Asn Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu
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VERIFICATION SUMMARY   DATE: 04/26/2001
PATENT APPLICATION: US/09/802,741   TIME: 10:40:03

Input Set : N:\Crf3\RULE60\09802741.txt
Output Set: N:\CRF3\04262001\I802741.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]